

**BLAST®** >> **blastn suite** >> results for RID-S4KKY2V0014

**Job Title** [Nucleotide Sequence ...](#)  
**RID** [S4KKY2V0014](#) Search expires on 09-19 23:34 pm  
**Program** BLASTN  
**Database** nr  
**Query ID** lcl|Query\_218683  
**Description** [None ...](#)  
**Molecule type** dna  
**Query Length** 1144

**Descriptions**

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630017O09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae), full insert sequence	1827	1827	87%	0.0	99.60%	<a href="#">AK154309.1</a>
PREDICTED: Mus musculus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1676	1676	87%	0.0	97.11%	<a href="#">XM_006510253.2</a>
Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Sc5d:tm1a(EUCOMM)Hmgu; transgenic	1676	1824	87%	0.0	97.11%	<a href="#">JN961338.1</a>
Mus musculus targeted non-conditional, lacZ-tagged mutant allele Sc5d:tm1e(EUCOMM)Hmgu; transgenic	1676	1824	87%	0.0	97.11%	<a href="#">JN951773.1</a>
Mus musculus sterol-C5-desaturase (Sc5d), mRNA	1676	1676	87%	0.0	97.11%	<a href="#">NM_172769.2</a>
Mus musculus BAC clone RP24-395P13 from chromosome 9, complete sequence	1676	1934	87%	0.0	97.11%	<a href="#">AC160051.2</a>
Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730515E09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae), full insert sequence	1676	1676	87%	0.0	97.11%	<a href="#">AK077670.1</a>
Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830037K02 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae), full insert sequence	1676	1676	87%	0.0	97.11%	<a href="#">AK043825.1</a>
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X3, mRNA	1520	1520	87%	0.0	94.31%	<a href="#">XM_029481771.1</a>
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	1520	1520	87%	0.0	94.31%	<a href="#">XM_021172472.2</a>
PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1520	1520	87%	0.0	94.31%	<a href="#">XM_021172471.1</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	1075	1075	87%	0.0	87.14%	<a href="#">XM_021207205.2</a>
Mus musculus C5D mRNA for sterol-C5-desaturase, complete cds	979	979	47%	0.0	99.44%	<a href="#">AB016248.1</a>
Mus musculus sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae), mRNA (cDNA clone MGC:37898 IMAGE:5101986), complete cds	977	977	46%	0.0	100.00%	<a href="#">BC024132.1</a>
PREDICTED: Rattus norvegicus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	732	732	87%	0.0	80.98%	<a href="#">XM_017595406.1</a>
Rattus norvegicus sterol-C5-desaturase (Sc5d), mRNA	732	732	87%	0.0	80.98%	<a href="#">NM_053642.2</a>
Mus musculus BAC clone RP23-346J12 from chromosome 6, complete sequence	702	796	54%	0.0	90.04%	<a href="#">AC122333.2</a>
PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	699	699	54%	0.0	87.84%	<a href="#">XM_021207206.2</a>
Mus musculus predicted gene, 31520 (Gm31520), non-coding RNA	678	678	46%	0.0	89.80%	<a href="#">NR_136927.1</a>
Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830041I17 product:weakly similar to STEROL C5-DESATURASE [Rattus norvegicus], full insert sequence	678	678	46%	0.0	89.80%	<a href="#">AK052921.1</a>
PREDICTED: Mus pahari lathosterol oxidase-like (LOC110334695), mRNA	579	579	46%	1e-160	87.25%	<a href="#">XM_029547953.1</a>
PREDICTED: Mesocricetus auratus sterol-C5-desaturase (Sc5d), mRNA	424	670	73%	6e-114	79.62%	<a href="#">XM_005069403.3</a>
Rattus norvegicus C5D mRNA for sterol C5-desaturase, complete cds	407	407	45%	6e-109	81.46%	<a href="#">AB052846.1</a>
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	396	396	50%	1e-105	79.44%	<a href="#">XM_007651891.3</a>
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	396	396	50%	1e-105	79.44%	<a href="#">XM_003511371.4</a>
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA	392	392	50%	2e-104	79.30%	<a href="#">XM_027411877.1</a>
PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA	392	392	50%	2e-104	79.30%	<a href="#">XM_027411876.1</a>
Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330029P19 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae), full insert sequence	259	259	13%	2e-64	96.79%	<a href="#">AK165139.1</a>
RNA interference vector psiCHECK(TM)-2, complete sequence	252	252	11%	3e-62	100.00%	<a href="#">AY535007.1</a>
RNA interference vector psiCHECK(TM)-1, complete sequence	252	252	11%	3e-62	100.00%	<a href="#">AY535006.1</a>
Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730048E03 product:unclassifiable, full insert sequence	241	241	13%	7e-59	95.39%	<a href="#">AK050439.1</a>
Co-reporter vector phRL-CMV, complete sequence	231	231	11%	4e-56	97.10%	<a href="#">AF362549.1</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Co-reporter vector phRL-SV40, complete sequence	231	231	11%	4e-56	97.10%	<a href="#">AF362548.1</a>
Co-reporter vector phRL-TK(Int-), complete sequence	231	231	11%	4e-56	97.10%	<a href="#">AF362547.1</a>
Co-reporter vector phRL-null, complete sequence	231	231	11%	4e-56	97.10%	<a href="#">AF362546.1</a>
Co-reporter vector pHRL-TK, complete sequence	231	231	11%	4e-56	97.10%	<a href="#">AF362545.1</a>
Renilla luciferase reporter vector pGL4.75[hRluc/CMV], complete sequence	228	228	10%	5e-55	100.00%	<a href="#">AY738231.1</a>
Renilla luciferase reporter vector pGL4.74[hRluc/TK], complete sequence	228	228	10%	5e-55	100.00%	<a href="#">AY738230.1</a>
Renilla luciferase reporter vector pGL4.73[hRluc/SV40], complete sequence	228	228	10%	5e-55	100.00%	<a href="#">AY738229.1</a>
Renilla luciferase reporter vector pGL4.70[hRluc], complete sequence	228	228	10%	5e-55	100.00%	<a href="#">AY738226.1</a>
Co-reporter vector phRG-TK, complete sequence	228	228	10%	5e-55	100.00%	<a href="#">AF362551.1</a>
Co-reporter vector phRG-B, complete sequence	228	228	10%	5e-55	100.00%	<a href="#">AF362550.1</a>
Synthetic Renilla luciferase reporter vector pGL4.82[hRluc/Puro], complete sequence	228	228	10%	5e-55	100.00%	<a href="#">DQ188846.1</a>
Renilla luciferase reporter vector pGL4.79[hRluc/Neo], complete sequence	228	228	10%	5e-55	100.00%	<a href="#">DQ188843.1</a>
Luciferase reporter vector pGL4.76[hRluc/Hygro], complete sequence	228	228	10%	5e-55	100.00%	<a href="#">AY864931.1</a>
Cloning vector pT7 RL2, complete sequence	217	217	10%	1e-51	100.00%	<a href="#">KM099240.1</a>
Cloning vector pT7_RL1, complete sequence	217	217	10%	1e-51	100.00%	<a href="#">KM099239.1</a>
Renilla luciferase reporter vector pGL4.72[hRlucCP], complete sequence	217	217	10%	1e-51	99.17%	<a href="#">AY738228.1</a>
Renilla luciferase reporter vector pGL4.71[hRlucP], complete sequence	217	217	10%	1e-51	99.17%	<a href="#">AY738227.1</a>
Reporter vector phRG(R2.2), complete sequence	217	217	10%	1e-51	99.17%	<a href="#">AY487824.1</a>
Reporter vector phRG(R2.1), complete sequence	217	217	10%	1e-51	99.17%	<a href="#">AY487823.1</a>
Synthetic Renilla luciferase reporter vector pGL4.84[hRlucCP/Puro], complete sequence	217	217	10%	1e-51	99.17%	<a href="#">DQ188848.1</a>
Synthetic Renilla luciferase reporter vector pGL4.83[hRlucP/Puro], complete sequence	217	217	10%	1e-51	99.17%	<a href="#">DQ188847.1</a>
Synthetic Renilla luciferase reporter vector pGL4.81[hRlucCP/Neo], complete sequence	217	217	10%	1e-51	99.17%	<a href="#">DQ188845.1</a>
Synthetic Renilla luciferase reporter vector pGL4.80[hRlucP/Neo], complete sequence	217	217	10%	1e-51	99.17%	<a href="#">DQ188844.1</a>
Luciferase reporter vector pGL4.78[hRlucCP/Hygro], complete sequence	217	217	10%	1e-51	99.17%	<a href="#">AY864933.1</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Luciferase reporter vector pGL4.77[hRlucP/Hygro], complete sequence	217	217	10%	1e-51	99.17%	<a href="#">AY864932.1</a>
Plant expression vector pDuExB2 (pDuExD7), complete sequence	213	425	10%	1e-50	100.00%	<a href="#">EF565885.1</a>
Plant expression vector pDuExB (pDuExDc6), complete sequence	213	213	10%	1e-50	100.00%	<a href="#">EF565884.1</a>
Synthetic construct clone Den3-E24 Rluc-ubiquitin-neo fusion protein and polyprotein genes, complete cds	211	211	9%	5e-50	100.00%	<a href="#">KM222446.1</a>
Synthetic construct clone Den3-E21 Rluc-ubiquitin-neo fusion protein and polyprotein genes, complete cds	211	211	9%	5e-50	100.00%	<a href="#">KM222445.1</a>
Cloning vector pCRm-Rluc-PHLEO, complete sequence	211	211	9%	5e-50	100.00%	<a href="#">KF035117.1</a>
Cloning vector pCRm-Rluc-PAC, complete sequence	211	211	9%	5e-50	100.00%	<a href="#">KF035116.1</a>
Cloning vector pCRm-Rluc-NEO, complete sequence	211	211	9%	5e-50	100.00%	<a href="#">KF035115.1</a>
Cloning vector pCRm-Rluc-HYG, complete sequence	211	211	9%	5e-50	100.00%	<a href="#">KF035114.1</a>
Cloning vector pCRm-Rluc-BSD, complete sequence	211	211	9%	5e-50	100.00%	<a href="#">KF035113.1</a>
Hepatitis C virus replicon 4a ED43-RlucNeo (R+I), complete sequence	211	211	9%	5e-50	100.00%	<a href="#">JX885981.1</a>
Biobrick cloning vector BBa_J96034, complete sequence	211	211	9%	5e-50	100.00%	<a href="#">JN204887.1</a>
Cloning vector pDuExDn6, complete sequence	211	211	9%	5e-50	100.00%	<a href="#">GU370779.1</a>
Cloning vector pBIND-GR, complete sequence	211	211	9%	5e-50	100.00%	<a href="#">GQ229580.1</a>
Cloning vector pBIND-ER (alpha), complete sequence	211	211	9%	5e-50	100.00%	<a href="#">GQ229579.1</a>
Cloning vector pFN26A (BIND) hRluc-neo, complete sequence	211	211	9%	5e-50	100.00%	<a href="#">GQ229578.1</a>
Cloning vector pmirGLO, complete sequence	211	211	9%	5e-50	100.00%	<a href="#">FJ376737.1</a>
CMV hRluc-neo Flexi Vector pF9A, complete sequence	211	211	9%	5e-50	100.00%	<a href="#">DQ871024.1</a>
Synthetic construct gene for mKusabiraOrangeKappa-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	<a href="#">LC033422.1</a>
Synthetic construct gene for mKusabiraOrange1-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	<a href="#">LC033416.1</a>
Synthetic construct gene for mCherry(delC13)-RLuc8.6(delN6), complete cds	206	206	10%	2e-48	98.29%	<a href="#">LC033414.1</a>
Synthetic construct gene for mCherry(delC13)-RLuc8.6(delN5), complete cds	206	206	10%	2e-48	98.29%	<a href="#">LC033413.1</a>
Synthetic construct gene for mCherry(delC13)-RLuc8.6(delN4), complete cds	206	206	10%	2e-48	98.29%	<a href="#">LC033412.1</a>
Synthetic construct gene for mCherry(delC12)-RLuc8.6(delN6), complete cds	206	206	10%	2e-48	98.29%	<a href="#">LC033411.1</a>

Description	Max Score	Total Score	Query Cover	E value	Per. Ident	Accession
Synthetic construct gene for mCherry(delC12)-RLuc8.6(delN5), complete cds	206	206	10%	2e-48	98.29%	<a href="#">LC033410.1</a>
Synthetic construct gene for mCherry(delC12)-RLuc8.6(delN4), complete cds	206	206	10%	2e-48	98.29%	<a href="#">LC033409.1</a>
Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6(delN6), complete cds	206	206	10%	2e-48	98.29%	<a href="#">LC033408.1</a>
Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6(delN5), complete cds	206	206	10%	2e-48	98.29%	<a href="#">LC033407.1</a>
Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6(delN4), complete cds	206	206	10%	2e-48	98.29%	<a href="#">LC033406.1</a>
Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	<a href="#">LC033405.1</a>
Synthetic construct gene for mCherry(delC10)-Orange-Nano-lantern, complete cds	206	206	10%	2e-48	98.29%	<a href="#">LC033404.1</a>
Synthetic construct gene for Che(dC10-sC2)-RL8m1, complete cds	206	206	10%	2e-48	98.29%	<a href="#">LC033401.1</a>
Synthetic construct gene for Che(dC10-sC1)-RL8m1, complete cds	206	206	10%	2e-48	98.29%	<a href="#">LC033400.1</a>
Synthetic construct gene for Orange-Nano-lantern(Ca2+)-H2B, complete cds	206	206	10%	2e-48	97.50%	<a href="#">AB983217.1</a>
Synthetic construct gene for Orange-Nano-lantern(Ca2+), complete cds	206	206	10%	2e-48	98.29%	<a href="#">AB983216.1</a>
Synthetic construct gene for TurboFP650-RLuc8.6-545, complete cds	206	206	10%	2e-48	98.29%	<a href="#">AB982104.1</a>
Synthetic construct gene for TurboFP635-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	<a href="#">AB982103.1</a>
Synthetic construct gene for TurboFP635-RLuc8.6-545, complete cds	206	206	10%	2e-48	98.29%	<a href="#">AB982102.1</a>
Synthetic construct gene for tdTomato-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	<a href="#">AB982100.1</a>
Synthetic construct gene for TagRFP-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	<a href="#">AB982098.1</a>
Synthetic construct gene for mRuby2-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	<a href="#">AB982096.1</a>
Synthetic construct gene for mOrange2-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	<a href="#">AB982095.1</a>
Synthetic construct gene for mKusabiraOrange2(delC5)-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	<a href="#">AB982094.1</a>
Synthetic construct gene for mKusabiraOrange2(delC4)-RLuc8.6, complete cds	206	206	10%	2e-48	98.29%	<a href="#">AB982093.1</a>

## Graphic Summary



Alignments

Alignment view 

Pairwise

☐ CDS feature

Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630017O09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisae), full insert sequence  
Sequence ID: **AK154309.1** Length: 2251 Number of Matches: 1  
Range 1: 1101 to 2102

Score	Expect	Identities	Gaps	Strand	Frame
1827 bits(989)	0.0()	998/1002(99%)	2/1002(0%)	Plus/Plus	
Query 145	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGT	CATGCTGAGGGATGGTCCTGACAGT	204		
Sbjct 1101	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGT	CATGCTGAGGGATGGTCCTGACAGT	1160		
Query 205	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	264			
Sbjct 1161	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	1220			
Query 265	AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	324			
Sbjct 1221	AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	1280			

Query	325	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT	384
Sbjct	1281	AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT	1340
Query	385	GCATACTCATTAAGGaaaaaaGTACCATTTGTGCTAAACGCTACTGAGACTAACCAGGAA	444
Sbjct	1341	GCATACTCATTAAGGAAAAAAAGTACCATTTGTGCTAAACGCTACTGAGACTAACCAGGAA	1400
Query	445	ACCCTAAAGATGAAGATGTTCTGTCCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA	504
Sbjct	1401	ACCCTAAAGATGAAGATGTTCTGTCCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA	1460
Query	505	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG	564
Sbjct	1461	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG	1520
Query	565	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCTTATACAGAGGCACCT	624
Sbjct	1521	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCTTATACAGAGGCACCT	1580
Query	625	TACTCTCTGGGGCATTATCAGATTTTAAATAAATGAATAAAATAAATGGTAattttttttAAA	684
Sbjct	1581	TACTCTCTGGGGCATTATCAGATTTTAAATAAATGAATAAAATAAATGGTATTTTTTTTAA	1640
Query	685	TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG	744
Sbjct	1641	TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG	1700
Query	745	AGTGTCAatttttttttcttttc--tttttttttttttttttttttttggttttttAAGACAG	802
Sbjct	1701	AGTGTCATTTTTTTTTCTTTCTTTTTTTTTTTTTTTTTTTTTTTTGGTTTTTTAAGACAG	1760
Query	803	GGTTTCTCTGTGTAGCCCTGGCTGTCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTC	862
Sbjct	1761	GGTTTCTCTGTGTAGCCCTGGCTGTCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTC	1820
Query	863	AGAGATCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCCTGCCAGCTTGATGT	922
Sbjct	1821	AGAGATCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCCTGCCAGCTTGATGT	1880
Query	923	GTGTCATTTAAAACCACTGTTTAAATAACCCCTACAGACATGAATCTGGATAATGCTAGGTA	982
Sbjct	1881	GTGTCATTTAAAACCACTGTTTAAATAACCCCTACAGACATGAATCTGGATAATGCTAGGTA	1940
Query	983	TAAACTTGTGGCACCAGTGACATCtttttttAATCAAGTGACACACTTTTGATGTATT	1042
Sbjct	1941	TAAACTTGTGGCACCAGTGACATCTTTTTTTAATCAAGTGACACACTTTTGATGTATT	2000
Query	1043	TCTCAGTTACAAAGCTGACTtttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTA	1102
Sbjct	2001	TCTCAGTTACAAAGCTGACTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTA	2060
Query	1103	CCTAAGGTACACTTTTAGACCTCATCTTCAATTTCTTCCCTCT	1144
Sbjct	2061	CCTAAGGTACACTTTTAGACCTCATCTTCTATTTCTTCCCTCT	2102

PREDICTED: Mus musculus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA

Sequence ID: **XM\_006510253.2** Length: 4826 Number of Matches: 1

Range 1: 1146 to 2133

Score	Expect	Identities	Gaps	Strand	Frame
1676 bits(907)	0.0()	973/1002(97%)	16/1002(1%)	Plus/Plus	
Query	145	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTGTCATGCTGAGGGATGGTCCTGACAGT	204		
Sbjct	1146	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTGTCATGCTGAGGGATGGTCCTGACAGT	1205		
Query	205	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	264		
Sbjct	1206	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	1265		
Query	265	AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	324		
Sbjct	1266	AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	1325		
Query	325	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT	384		
Sbjct	1326	AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCCTTTTGCCTTAGTCCAT	1385		
Query	385	GCATACTCATTAAGGaaaaaaGTACCATTTGTGCTAAACGCTACTGAGACTAACCAGGAA	444		
Sbjct	1386	GCATACTCATTAAGGAAAAAAAGTACCATTTGTGCTAAACGCTACTGAGACTAACCAGGAA	1445		
Query	445	ACCCTAAAGATGAAGATGTTCTGTCCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA	504		

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Sbjct  1446  ACCCTAACGATGAAGATGGTCCTGTCCCGGAGCGGCTGGCTCCACCGAAGTGCCTGGGGA  1505
Query   505    GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG  564
Sbjct  1506    GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAAGCTGATACGTGAGTGGCAG  1565
Query   565    TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT  624
Sbjct  1566    TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT  1625
Query   625    TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTAttttttttAAA  684
Sbjct  1626    TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTATTTTTTTTAA  1685
Query   685    TGTCAGCTCTTCCATAATTCAAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG  744
Sbjct  1686    TGTCAGCTCTTCCATAATTCAAGTCTAGATAGGAGATTATTTAACTGAAGA--TCTTGGTG  1743
Query   745    AGTGTCAAtttttttttctttcttttttttttttttttttttttggttttttAAGACAGGG  804
Sbjct  1744    AGTGTCAATTTTTTTTCTTT-TTTC-----TTTTTTTGGTTTTTCAAGACAGGG  1791
Query   805    TTTCTCTGTGTAGCCCTGGCTGTCTCGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAG  864
Sbjct  1792    TTTCTCTGTGTAGCCCTGGCTGTCTCGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAG  1851
Query   865    AGATCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCCTGCCAGCTTGATGTGT  924
Sbjct  1852    AGATCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCCTGCCAGCTTGAAGTGT  1911
Query   925    GTCATTTAAAACCACTGTTTAATAACCCCTACAGACATGAATCTGGATAATGCTAGGTATA  984
Sbjct  1912    GTCATTTAAAACCACTGTTTAATAACCCCTACAGACATGAATCTGGATAATGCTAGGTATA  1971
Query   985    AACTTGTGGCACCCAGTGACATCtttttttAATCAAGTGGACACACTTTTGATGTATTC  1044
Sbjct  1972    AACTTGTGGCACCCAGTGACATCTTTTTTAAATCAAGTGGACACACTTTTGATGTATTC  2031
Query  1045    TCAGTTACAAAGCTGAC-tttttttAATGAAGGAATAATTGCCAAGTACTTAAATCTAC  1103
Sbjct  2032    TCAGTTACAAAGCTGACTTTTTTTTAAATGAAGGAATAATTGCCAAGTACTTAAATCTAC  2091
Query  1104    CTAAGGTACAC-TTTAGACCTCATCTTCAATTTCTTCCCTCT  1144
Sbjct  2092    CTGAGGTACACTTTTAAACCTCATCTTCTATTTCTTCCCTCT  2133

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Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Sc5d:tm1a(EUCOMM)Hmgu; transgenic

Sequence ID: **JN961338.1** Length: 38137 Number of Matches: 2

Range 1: 26029 to 27016

Score	Expect	Identities	Gaps	Strand	Frame
1676 bits(907)	0.0()	973/1002(97%)	16/1002(1%)	Plus/Plus	
Query 145	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTGATGCTGAGGGATGGTCTTGACAGT	204			
Sbjct 26029	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTGATGCTGAGGGATGGTCTTGACAGT	26088			
Query 205	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	264			
Sbjct 26089	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	26148			
Query 265	AGGAACAACCTTGCTTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	324			
Sbjct 26149	AGGAACAACCTTGCTTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	26208			
Query 325	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT	384			
Sbjct 26209	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT	26268			
Query 385	GCATACTCATTAAGGaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA	444			
Sbjct 26269	GCATACTCATTAAGGAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA	26328			
Query 445	ACCCTAAAGATGAAGATGTTCTGTCCCGGAGCGGCTGGCTCCACCGCAGTGCTGGGGA	504			
Sbjct 26329	ACCCTAACGATGAAGATGGTCTGTCCCGGAGCGGCTGGCTCCACCGAAGTGCTGGGGA	26388			
Query 505	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG	564			
Sbjct 26389	GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAAGCTGATACGTGAGTGGCAG	26448			
Query 565	TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT	624			



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Sbjct  26449  TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCCTATACAGAGGCACCT 26508
Query   625    TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAAATAAATGGTAatTTTTTTAAA 684
Sbjct  26509  TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAAATAAATGGTATTTTTTTTAAA 26568
Query   685    TGTACAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG 744
Sbjct  26569  TGTACAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA--TCTTGGTG 26626
Query   745    AGTGTCAatTTTTTTTTctttctTTTTTTTTTTTTTTTTTTTTTTTTTggtTTTTAAGACAGGG 804
Sbjct  26627  AGTGTCAATTTTTTTTTCTTT-TTTC-----TTTTTTTGGTTTTTCAAGACAGGG 26674
Query   805    TTTCTCTGTGTAGCCCTGGCTGTCTTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAG 864
Sbjct  26675  TTTCTCTGTGTAGCCCTGGCTGTCTTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAG 26734
Query   865    AGATCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACAGCCAGCTTGATGTGT 924
Sbjct  26735  AGATCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACAGCCAGCTTGAAGTGT 26794
Query   925    GTCATTTAAACCACCTGTTTAATAACCCCTACAGACATGAATCTGGATAATGCTAGGTATA 984
Sbjct  26795  GTCATTTAAACCACCTGTTTAATAACCCCTACAGACATGAATCTGGATAATGCTAGGTATA 26854
Query   985    AACTTGTGGCACCAGTGACATCtTTTTTTAATCAAGTGGACACACTTTTGATGTATTTTC 1044
Sbjct  26855  AACTTGTGGCACCAGTGACATCTTTTTTAAATCAAGTGGACACACTTTTGATGTATTTTC 26914
Query  1045    TCAGTTACAAAGCTGAC-tTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTAC 1103
Sbjct  26915  TCAGTTACAAAGCTGACTTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTAC 26974
Query  1104    CTAAGGTACAC-TTTAGACCTCATCTTCAATTTCTTCCCTCT 1144
Sbjct  26975  CTGAGGTACACTTTTAAACCTCATCTTCTATTTCCTTCCCTCT 27016

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Range 2: 37069 to 37200

Score	Expect	Identities	Gaps	Strand	Frame
148 bits(80)	4e-31()	116/132(88%)	7/132(5%)	Plus/Plus	
Query 753	ttttttttctttcttttttttt-tttttttt-tttt-tttggttttttAAGACAGGGTTTCT	809			
Sbjct 37069	TTTTTTTGCTTTTTGTTTTTGTTTTTGTTTTTGTTTTTGTTTTTTAAGACAGGGTTTCT	37128			
Query 810	CTGTGTAGCCCTGGCTGTCTTGGAACTC--T--GTAGACTGGGCTGGCCTCGAACTCAGA	865			
Sbjct 37129	CTGTGTAGCCCTGGCTGTCTTGGAGCTCACTTTGTAGATCAGGCTGGCCTCGAACTCAGA	37188			
Query 866	GATCTGCCTGCC 877				
Sbjct 37189	AATCTGCCTGCC 37200				

Mus musculus targeted non-conditional, lacZ-tagged mutant allele Sc5d:tm1e(EUCOMM)Hmgu; transgenic

Sequence ID: **JN951773.1** Length: 38097 Number of Matches: 2

Range 1: 25989 to 26976

Score	Expect	Identities	Gaps	Strand	Frame
1676 bits(907)	0.0()	973/1002(97%)	16/1002(1%)	Plus/Plus	
Query 145	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTGTCATGCTGAGGGATGGTCCTGACAGT	204			
Sbjct 25989	GTGGTGCCATTGGAATGTCAGCATTGCTTGAGTGTGTCATGCTGAGGGATGGTCCTGACAGT	26048			
Query 205	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	264			
Sbjct 26049	AAACAGCGGGAAGACACCAGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC	26108			
Query 265	AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	324			
Sbjct 26109	AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT	26168			
Query 325	AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT	384			
Sbjct 26169	AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT	26228			
Query 385	GCATACTCATTAAGGaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA	444			

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Sbjct  26229  GCATACTCATTAAAGGAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA 26288
Query   445     ACCCTAAAGATGAAGATGTTCTGTCCCCGAGCGGCTGGCTCCACCGCAGTGCTGGGGA 504
Sbjct  26289  ACCCTAACGATGAAGATGGTCTGTCCCCGAGCGGCTGGCTCCACCGAAGTGCTGGGGA 26348
Query   505     GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGGCAG 564
Sbjct  26349  GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAAGCTGATACGTGAGTGGCAG 26408
Query   565     TGGATAGGATTTTGCTTAATGGCTGATGTAATAAGATTGTACTTCTTATACAGAGGCACCT 624
Sbjct  26409  TGGATAGGATTTTGCTTAATGGCTGATGTAATAAGATTGTACTTCTTATACAGAGGCACCT 26468
Query   625     TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTA ttttttttAAA 684
Sbjct  26469  TACTCTCTGGGGCATTATCAGATTTTAATAAATGAATAAATAAATGGTATTTTTTTTAAA 26528
Query   685     TGTCACTCTTCCATAATTCACTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG 744
Sbjct  26529  TGTCACTCTTCCATAATTCACTCTAGATAGGAGATTATTTAACTGAAGA--TCTTGGTG 26586
Query   745     AGTGTCA tttttttttctttcttttttttttttttttttttttggttttttAAGACAGGG 804
Sbjct  26587  AGTGTCA TTTTTTTTCTTT-TTTC-----TTTTTTTGGTTTTTCAAGACAGGG 26634
Query   805     TTTCTCTGTGTAGCCCTGGCTGTCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAG 864
Sbjct  26635  TTTCTCTGTGTAGCCCTGGCTGTCTGGAACCTCTGTAGACTGGGCTGGCCTCGAACTCAG 26694
Query   865     AGATCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACCTGCCAGCTTGATGTGT 924
Sbjct  26695  AGATCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCACCTGCCAGCTTGAAGTGT 26754
Query   925     GTCATTTAAACCCTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATA 984
Sbjct  26755  GTCATTTAAACCCTGTTTAATAACCCTACAGACATGAATCTGGATAATGCTAGGTATA 26814
Query   985     AACTTGTGGCACCCAGTGACATC ttttttttAATCAAGTGGACACACTTTTGATGTATTTC 1044
Sbjct  26815  AACTTGTGGCACCCAGTGACATC TTTTTTTAATCAAGTGGACACACTTTTGATGTATTTC 26874
Query  1045     TCAGTTACAAAGCTGAC-ttttttttAATGAAGGGAATAATTGCCAAGTACTTAAATCTAC 1103
Sbjct  26875  TCAGTTACAAAGCTGACTTTTTTTTAAATGAAGGGAATAATTGCCAAGTACTTAAATCTAC 26934
Query  1104     CTAAGGTACAC-TTTAGACCTCATCTTCAATTTCTTCCCTCT 1144
Sbjct  26935  CTGAGGTACACTTTTAAACCTCATCTTCTATTTCCTTCCCTCT 26976

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Range 2: 37029 to 37160

Score	Expect	Identities	Gaps	Strand	Frame
148 bits(80)	4e-31()	116/132(88%)	7/132(5%)	Plus/Plus	
Query 753	ttttttttctttcttttttttt-tttttttt-tttt-tttggttttttAAGACAGGGTTTCT	809			
Sbjct 37029	TTTTTTTGCTTTTTTGTTTTTGTTTTTGTTTTTGTTTTGTTTTTAAAGACAGGGTTTCT	37088			
Query 810	CTGTGTAGCCCTGGCTGTCTGGAACCT--T--GTAGACTGGGCTGGCCTCGAACTCAGA	865			
Sbjct 37089	CTGTGTAGCCCTGGCTGTCTGGAGCTCACTTTGTAGATCAGGCTGGCCTCGAACTCAGA	37148			
Query 866	GATCTGCCTGCC 877				
Sbjct 37149	AATCTGCCTGCC 37160				

Mus musculus sterol-C5-desaturase (Sc5d), mRNA

Sequence ID: **NM\_172769.2** Length: 2249 Number of Matches: 1

Range 1: 1154 to 2141

Score	Expect	Identities	Gaps	Strand	Frame
1676 bits(907)	0.0()	973/1002(97%)	16/1002(1%)	Plus/Plus	
Query 145	GTGGTGCCATTGGAATGTCAGCATTTGCTTGAGTGTATGCTGAGGGATGGTCCTGACAGT	204			
Sbjct 1154	GTGGTGCCATTGGAATGTCAGCATTTGCTTGAGTGTATGCTGAGGGATGGTCCTGACAGT	1213			
Query 205	AAACAGCGGGAAGACACCAGGAGCATTTGAATCGCTTGGTTAATTGTCCGACATTGGTCC	264			

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Sbjct 1214 AAACAGCGGGAAGACACCGGGAGCATTGTAATCGCTTGGTTAATTGTCCGACATTGGTCC 1273
Query 265 AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT 324
Sbjct 1274 AGGAACAACCTTGTCTTTTCAGCCGGCTGACCTGCAGCCTGTACAGCTCTGAAGCATCTTT 1333
Query 325 AAATACGATAGAAAATAAGTTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT 384
Sbjct 1334 AAATACGATAGAAAATAAGCTACTCAAGAAGCTGGTCTGTGTCTTTTGCCTTAGTCCAT 1393
Query 385 GCATACTCATTAAGGaaaaaaaGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA 444
Sbjct 1394 GCATACTCATTAAGGAAAAAAAGTACCATTGTGCTAAACGCTACTGAGACTAACCAGGAA 1453
Query 445 ACCCTAAAGATGAAGATGTTCTGTCCCGGAGCGGTGGCTCCACCGCAGTGCTGGGGA 504
Sbjct 1454 ACCCTAACGATGAAGATGGTCTGTCCCGGAGCGGTGGCTCCACCGAAGTGCTGGGGA 1513
Query 505 GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGCGAG 564
Sbjct 1514 GTTGCAGGACTTCATTCAAATAGGAATATCAGTCCAAGCAGGCTGATACGTGAGTGCGAG 1573
Query 565 TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCTTATACAGAGGCACCT 624
Sbjct 1574 TGGATAGGATTTGCTTAATGGCTGATGTAATAAGATTGTACTTCTTATACAGAGGCACCT 1633
Query 625 TACTCTCTGGGGCATTATCAGATTTTAAATAAATGAATAAATAAATGGTAatTTTTTTTAAA 684
Sbjct 1634 TACTCTCTGGGGCATTATCAGATTTTAAATAAATGAATAAATAAATGGTATTTTTTTTAAA 1693
Query 685 TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGATCTCTTGGTG 744
Sbjct 1694 TGTCAGCTCTTCCATAATTCAGTCTAGATAGGAGATTATTTAACTGAAGA--TCTTGGTG 1751
Query 745 AGTGTCAatTTTTTTTctttctTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTgTTTTTtAAGACAGGG 804
Sbjct 1752 AGTGTCATTTTTTTTTCTTT-TTTC-----TTTTTTTGGTTTTTCAAGACAGGG 1799
Query 805 TTTCTCTGTGTAGCCCTGGCTGTCTTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAG 864
Sbjct 1800 TTTCTCTGTGTAGCCCTGGCTGTCTTGGAACTCTGTAGACTGGGCTGGCCTCGAACTCAG 1859
Query 865 AGATCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCCTGCCAGCTTGATGTGT 924
Sbjct 1860 AGATCTGCCTGCCCTTGCTGGGATCAGAGGTGTGCACCACCCTGCCAGCTTGAAAGTGT 1919
Query 925 GTCATTTAAAACCACTGTTTAATAACCCACAGACATGAATCTGGATAATGCTAGGTATA 984
Sbjct 1920 GTCATTTAAAACCACTGTTTAATAACCCACAGACATGAATCTGGATAATGCTAGGTATA 1979
Query 985 AACTTGTGGCACCCAGTGACATCtTTTTTTtAATCAAGTGGACACACTTTTGATGTATTTT 1044
Sbjct 1980 AACTTGTGGCACCCAGTGACATCTTTTTTTAATCAAGTGGACACACTTTTGATGTATTTT 2039
Query 1045 TCAGTTACAAAGCTGAC-tTTTTTTtAATGAAGGGAATAATTGCCAAGTACTTAAATCTAC 1103
Sbjct 2040 TCAGTTACAAAGCTGACTTTTTTTTTAATGAAGGGAATAATTGCCAAGTACTTAAATCTAC 2099
Query 1104 CTAAGGTACAC-TTTAGACCTCATCTTCAATTTCTTCCCTCT 1144
Sbjct 2100 CTGAGGTACACTTTTAAACCTCATCTTCTATTTCTTCCCTCT 2141

```

## Taxonomy

### Reports

#### ◦ Lineage

Organism	Blast Name	Score	Number of Hits	Description
<a href="#">root</a>			<a href="#">101</a>	
<a href="#">.Muroidea</a>	<a href="#">rodents</a>		<a href="#">30</a>	
<a href="#">..Murinae</a>	<a href="#">rodents</a>		<a href="#">25</a>	
<a href="#">...Mus</a>	<a href="#">rodents</a>		<a href="#">21</a>	
<a href="#">....Mus</a>	<a href="#">rodents</a>		<a href="#">18</a>	
<a href="#">.....Mus musculus</a>	<a href="#">rodents</a>	1827	<a href="#">15</a>	<a href="#">Mus musculus hits</a>

<a href="#">....Mus caroli</a>	<a href="#">rodents</a>	1520	<a href="#">3</a>	<a href="#">Mus caroli hits</a>
<a href="#">....Mus pahari</a>	<a href="#">rodents</a>	1075	<a href="#">3</a>	<a href="#">Mus pahari hits</a>
<a href="#">...Rattus norvegicus</a>	<a href="#">rodents</a>	732	<a href="#">4</a>	<a href="#">Rattus norvegicus hits</a>
<a href="#">..Mesocricetus auratus</a>	<a href="#">rodents</a>	424	<a href="#">1</a>	<a href="#">Mesocricetus auratus hits</a>
<a href="#">..Cricetulus griseus</a>	<a href="#">rodents</a>	396	<a href="#">4</a>	<a href="#">Cricetulus griseus hits</a>
<a href="#">.RNA interference vector psiCHECK(TM)-2</a>	<a href="#">other sequences</a>	252	<a href="#">1</a>	<a href="#">RNA interference vector psiCHECK(TM)-2 hits</a>
<a href="#">.RNA interference vector psiCHECK(TM)-1</a>	<a href="#">other sequences</a>	252	<a href="#">1</a>	<a href="#">RNA interference vector psiCHECK(TM)-1 hits</a>
<a href="#">.Co-reporter vector phRL-CMV</a>	<a href="#">other sequences</a>	231	<a href="#">1</a>	<a href="#">Co-reporter vector phRL-CMV hits</a>
<a href="#">.Co-reporter vector phRL-SV40</a>	<a href="#">other sequences</a>	231	<a href="#">1</a>	<a href="#">Co-reporter vector phRL-SV40 hits</a>
<a href="#">.Co-reporter vector phRL-TK(Int-)</a>	<a href="#">other sequences</a>	231	<a href="#">1</a>	<a href="#">Co-reporter vector phRL-TK(Int-) hits</a>
<a href="#">.Co-reporter vector phRL-null</a>	<a href="#">other sequences</a>	231	<a href="#">1</a>	<a href="#">Co-reporter vector phRL-null hits</a>
<a href="#">.Co-reporter vector pHRL-TK</a>	<a href="#">other sequences</a>	231	<a href="#">1</a>	<a href="#">Co-reporter vector pHRL-TK hits</a>
<a href="#">.Renilla luciferase reporter vector pGL4.75[hRluc/CMV]</a>	<a href="#">other sequences</a>	228	<a href="#">1</a>	<a href="#">Renilla luciferase reporter vector pGL4.75[hRluc/CMV] hits</a>
<a href="#">.Renilla luciferase reporter vector pGL4.74[hRluc/TK]</a>	<a href="#">other sequences</a>	228	<a href="#">1</a>	<a href="#">Renilla luciferase reporter vector pGL4.74[hRluc/TK] hits</a>
<a href="#">.Renilla luciferase reporter vector pGL4.73[hRluc/SV40]</a>	<a href="#">other sequences</a>	228	<a href="#">1</a>	<a href="#">Renilla luciferase reporter vector pGL4.73[hRluc/SV40] hits</a>
<a href="#">.Renilla luciferase reporter vector pGL4.70[hRluc]</a>	<a href="#">other sequences</a>	228	<a href="#">1</a>	<a href="#">Renilla luciferase reporter vector pGL4.70[hRluc] hits</a>
<a href="#">.Co-reporter vector phRG-TK</a>	<a href="#">other sequences</a>	228	<a href="#">1</a>	<a href="#">Co-reporter vector phRG-TK hits</a>
<a href="#">.Co-reporter vector phRG-B</a>	<a href="#">other sequences</a>	228	<a href="#">1</a>	<a href="#">Co-reporter vector phRG-B hits</a>
<a href="#">.Renilla luciferase reporter vector pGL4.82[hRluc/Puro]</a>	<a href="#">other sequences</a>	228	<a href="#">1</a>	<a href="#">Renilla luciferase reporter vector pGL4.82[hRluc/Puro] hits</a>
<a href="#">.Renilla luciferase reporter vector pGL4.79[hRluc/Neo]</a>	<a href="#">other sequences</a>	228	<a href="#">1</a>	<a href="#">Renilla luciferase reporter vector pGL4.79[hRluc/Neo] hits</a>
<a href="#">.Luciferase reporter vector pGL4.76[hRluc/Hygro]</a>	<a href="#">other sequences</a>	228	<a href="#">1</a>	<a href="#">Luciferase reporter vector pGL4.76[hRluc/Hygro] hits</a>
<a href="#">.Cloning vector pT7 RL2</a>	<a href="#">other sequences</a>	217	<a href="#">1</a>	<a href="#">Cloning vector pT7 RL2 hits</a>
<a href="#">.Cloning vector pT7 RL1</a>	<a href="#">other sequences</a>	217	<a href="#">1</a>	<a href="#">Cloning vector pT7 RL1 hits</a>
<a href="#">.Renilla luciferase reporter vector pGL4.72[hRlucCP]</a>	<a href="#">other sequences</a>	217	<a href="#">1</a>	<a href="#">Renilla luciferase reporter vector pGL4.72[hRlucCP] hits</a>
<a href="#">.Renilla luciferase reporter vector pGL4.71[hRlucP]</a>	<a href="#">other sequences</a>	217	<a href="#">1</a>	<a href="#">Renilla luciferase reporter vector pGL4.71[hRlucP] hits</a>
<a href="#">.Reporter vector phRG(R2.2)</a>	<a href="#">other sequences</a>	217	<a href="#">1</a>	<a href="#">Reporter vector phRG(R2.2) hits</a>
<a href="#">.Reporter vector phRG(R2.1)</a>	<a href="#">other sequences</a>	217	<a href="#">1</a>	<a href="#">Reporter vector phRG(R2.1) hits</a>
<a href="#">.Renilla luciferase reporter vector pGL4.84[hRlucCP/Puro]</a>	<a href="#">other sequences</a>	217	<a href="#">1</a>	<a href="#">Renilla luciferase reporter vector pGL4.84[hRlucCP/Puro] hits</a>
<a href="#">.Renilla luciferase reporter vector pGL4.83[hRlucP/Puro]</a>	<a href="#">other sequences</a>	217	<a href="#">1</a>	<a href="#">Renilla luciferase reporter vector pGL4.83[hRlucP/Puro] hits</a>
<a href="#">.Renilla luciferase reporter vector pGL4.81[hRlucCP/Neo]</a>	<a href="#">other sequences</a>	217	<a href="#">1</a>	<a href="#">Renilla luciferase reporter vector pGL4.81[hRlucCP/Neo] hits</a>
<a href="#">.Renilla luciferase reporter vector</a>	<a href="#">other</a>	217	<a href="#">1</a>	<a href="#">Renilla luciferase reporter vector</a>

<a href="#">pGL4.80[hRlucP/Neo]</a>	<a href="#">sequences</a>			<a href="#">pGL4.80[hRlucP/Neo] hits</a>
<a href="#">.Luciferase reporter vector pGL4.78[hRlucCP/Hygro]</a>	<a href="#">other sequences</a>	217	<a href="#">1</a>	<a href="#">Luciferase reporter vector pGL4.78[hRlucCP/Hygro] hits</a>
<a href="#">.Luciferase reporter vector pGL4.77[hRlucP/Hygro]</a>	<a href="#">other sequences</a>	217	<a href="#">1</a>	<a href="#">Luciferase reporter vector pGL4.77[hRlucP/Hygro] hits</a>
<a href="#">.Plant expression vector pDuExB2 (pDuExD7)</a>	<a href="#">other sequences</a>	213	<a href="#">1</a>	<a href="#">Plant expression vector pDuExB2 (pDuExD7) hits</a>
<a href="#">.Plant expression vector pDuExB (pDuExDc6)</a>	<a href="#">other sequences</a>	213	<a href="#">1</a>	<a href="#">Plant expression vector pDuExB (pDuExDc6) hits</a>
<a href="#">.synthetic construct</a>	<a href="#">other sequences</a>	211	<a href="#">28</a>	<a href="#">synthetic construct hits</a>
<a href="#">.Cloning vector pCRm-Rluc-PHLEO</a>	<a href="#">other sequences</a>	211	<a href="#">1</a>	<a href="#">Cloning vector pCRm-Rluc-PHLEO hits</a>
<a href="#">.Cloning vector pCRm-Rluc-PAC</a>	<a href="#">other sequences</a>	211	<a href="#">1</a>	<a href="#">Cloning vector pCRm-Rluc-PAC hits</a>
<a href="#">.Cloning vector pCRm-Rluc-NEO</a>	<a href="#">other sequences</a>	211	<a href="#">1</a>	<a href="#">Cloning vector pCRm-Rluc-NEO hits</a>
<a href="#">.Cloning vector pCRm-Rluc-HYG</a>	<a href="#">other sequences</a>	211	<a href="#">1</a>	<a href="#">Cloning vector pCRm-Rluc-HYG hits</a>
<a href="#">.Cloning vector pCRm-Rluc-BSD</a>	<a href="#">other sequences</a>	211	<a href="#">1</a>	<a href="#">Cloning vector pCRm-Rluc-BSD hits</a>
<a href="#">.Hepatitis C virus replicon 4a ED43-RlucNeo (R+I)</a>	<a href="#">other sequences</a>	211	<a href="#">1</a>	<a href="#">Hepatitis C virus replicon 4a ED43-RlucNeo (R+I) hits</a>
<a href="#">.Biobrick cloning vector BBa_J96034</a>	<a href="#">other sequences</a>	211	<a href="#">1</a>	<a href="#">Biobrick cloning vector BBa_J96034 hits</a>
<a href="#">.Cloning vector pDuExDn6</a>	<a href="#">other sequences</a>	211	<a href="#">1</a>	<a href="#">Cloning vector pDuExDn6 hits</a>
<a href="#">.Cloning vector pBIND-GR</a>	<a href="#">other sequences</a>	211	<a href="#">1</a>	<a href="#">Cloning vector pBIND-GR hits</a>
<a href="#">.Cloning vector pBIND-ER (alpha)</a>	<a href="#">other sequences</a>	211	<a href="#">1</a>	<a href="#">Cloning vector pBIND-ER (alpha) hits</a>
<a href="#">.Cloning vector pFN26A (BIND) hRluc-neo</a>	<a href="#">other sequences</a>	211	<a href="#">1</a>	<a href="#">Cloning vector pFN26A (BIND) hRluc-neo hits</a>
<a href="#">.Cloning vector pmirGLO</a>	<a href="#">other sequences</a>	211	<a href="#">1</a>	<a href="#">Cloning vector pmirGLO hits</a>
<a href="#">.CMV hRluc-neo Flexi Vector pF9A</a>	<a href="#">other sequences</a>	211	<a href="#">1</a>	<a href="#">CMV hRluc-neo Flexi Vector pF9A hits</a>

## o Organism

Description	Score	E value	Accession
Mus musculus (house mouse) [rodents ]			
<a href="#">Mus musculus NOD-derived CD11c +ve dendritic cells cDNA, RIKEN full-length enriched library, clone:F630017O09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog (S. cerevisiae), full insert sequence</a>	1827	0.0	<a href="#">AK154309</a>
<a href="#">PREDICTED: Mus musculus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA</a>	1676	0.0	<a href="#">XM_006510253</a>
<a href="#">Mus musculus targeted KO-first, conditional ready, lacZ-tagged mutant allele Sc5d:tm1a(EUCOMM)Hmgq; transgenic</a>	1676	0.0	<a href="#">JN961338</a>
<a href="#">Mus musculus targeted non-conditional, lacZ-tagged mutant allele Sc5d:tm1e(EUCOMM)Hmgq; transgenic</a>	1676	0.0	<a href="#">JN951773</a>
<a href="#">Mus musculus sterol-C5-desaturase (Sc5d), mRNA</a>	1676	0.0	<a href="#">NM_172769</a>
<a href="#">Mus musculus BAC clone RP24-395P13 from chromosome 9, complete sequence</a>	1676	0.0	<a href="#">AC160051</a>

Description	Score	E value	Accession
<a href="#">Mus musculus 8 days embryo whole body cDNA, RIKEN full-length enriched library, clone:5730515E09 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog.(S. cerevisiae), full insert sequence</a>	1676	0.0	<a href="#">AK077670</a>
<a href="#">Mus musculus 10 days neonate cortex cDNA, RIKEN full-length enriched library, clone:A830037K02 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog.(S. cerevisiae), full insert sequence</a>	1676	0.0	<a href="#">AK043825</a>
<a href="#">Mus musculus C5D mRNA for sterol-C5-desaturase, complete cds</a>	979	0.0	<a href="#">AB016248</a>
<a href="#">Mus musculus sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog.(S. cerevisiae), mRNA (cDNA clone MGC:37898 IMAGE:5101986), complete cds</a>	977	0.0	<a href="#">BC024132</a>
<a href="#">Mus musculus BAC clone RP23-346J12 from chromosome 6, complete sequence</a>	702	0.0	<a href="#">AC122333</a>
<a href="#">Mus musculus predicted gene, 31520 (Gm31520), non-coding RNA</a>	678	0.0	<a href="#">NR_136927</a>
<a href="#">Mus musculus 16 days neonate heart cDNA, RIKEN full-length enriched library, clone:D830041I17 product:weakly similar to STEROL C5-DESATURASE [Rattus norvegicus], full insert sequence</a>	678	0.0	<a href="#">AK052921</a>
<a href="#">Mus musculus 2 days pregnant adult female ovary cDNA, RIKEN full-length enriched library, clone:E330029P19 product:sterol-C5-desaturase (fungal ERG3, delta-5-desaturase) homolog.(S. cerevisiae), full insert sequence</a>	259	2e-64	<a href="#">AK165139</a>
<a href="#">Mus musculus adult male liver tumor cDNA, RIKEN full-length enriched library, clone:C730048E03 product:unclassifiable, full insert sequence</a>	241	7e-59	<a href="#">AK050439</a>
Mus caroli (Ryukyu mouse) [rodents ]			
<a href="#">PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X3, mRNA</a>	1520	0.0	<a href="#">XM_029481771</a>
<a href="#">PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA</a>	1520	0.0	<a href="#">XM_021172472</a>
<a href="#">PREDICTED: Mus caroli sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA</a>	1520	0.0	<a href="#">XM_021172471</a>
Mus pahari (shrew mouse) [rodents ]			
<a href="#">PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA</a>	1075	0.0	<a href="#">XM_021207205</a>
<a href="#">PREDICTED: Mus pahari sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA</a>	699	0.0	<a href="#">XM_021207206</a>
<a href="#">PREDICTED: Mus pahari lathosterol oxidase-like (LOC110334695), mRNA</a>	579	1e-160	<a href="#">XM_029547953</a>
Rattus norvegicus (Norway rat) [rodents ]			
<a href="#">PREDICTED: Rattus norvegicus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA</a>	732	0.0	<a href="#">XM_017595406</a>
<a href="#">Rattus norvegicus sterol-C5-desaturase (Sc5d), mRNA</a>	732	0.0	<a href="#">NM_053642</a>
<a href="#">Rattus norvegicus sterol-C5-desaturase (ERG3 delta-5-desaturase homolog, S. cerevisiae)-like, mRNA (cDNA clone MGC:93101 IMAGE:7131154), complete cds</a>	732	0.0	<a href="#">BC081704</a>
<a href="#">Rattus norvegicus C5D mRNA for sterol C5-desaturase, complete cds</a>	407	6e-109	<a href="#">AB052846</a>
Mesocricetus auratus (golden hamster) [rodents ]			
<a href="#">PREDICTED: Mesocricetus auratus sterol-C5-desaturase (Sc5d), mRNA</a>	424	6e-114	<a href="#">XM_005069403</a>
Cricetulus griseus (Chinese hamster) [rodents ]			
<a href="#">PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA</a>	396	1e-105	<a href="#">XM_007651891</a>
<a href="#">PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA</a>	396	1e-105	<a href="#">XM_003511371</a>
<a href="#">PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X2, mRNA</a>	392	2e-104	<a href="#">XM_027411877</a>
<a href="#">PREDICTED: Cricetulus griseus sterol-C5-desaturase (Sc5d), transcript variant X1, mRNA</a>	392	2e-104	<a href="#">XM_027411876</a>
RNA interference vector psiCHECK(TM)-2 [other sequences ]			
<a href="#">RNA interference vector psiCHECK(TM)-2, complete sequence</a>	252	3e-62	<a href="#">AY535007</a>
RNA interference vector psiCHECK(TM)-1 [other sequences ]			
<a href="#">RNA interference vector psiCHECK(TM)-1, complete sequence</a>	252	3e-62	<a href="#">AY535006</a>
Co-reporter vector phRL-CMV [other sequences ]			

Description	Score	E value	Accession
<a href="#">Co-reporter vector phRL-CMV, complete sequence</a>	231	4e-56	<a href="#">AF362549</a>
Co-reporter vector phRL-SV40 [other sequences ]			
<a href="#">Co-reporter vector phRL-SV40, complete sequence</a>	231	4e-56	<a href="#">AF362548</a>
Co-reporter vector phRL-TK(Int-) [other sequences ]			
<a href="#">Co-reporter vector phRL-TK(Int-), complete sequence</a>	231	4e-56	<a href="#">AF362547</a>
Co-reporter vector phRL-null [other sequences ]			
<a href="#">Co-reporter vector phRL-null, complete sequence</a>	231	4e-56	<a href="#">AF362546</a>
Co-reporter vector pHRL-TK [other sequences ]			
<a href="#">Co-reporter vector pHRL-TK, complete sequence</a>	231	4e-56	<a href="#">AF362545</a>
Renilla luciferase reporter vector pGL4.75[hRluc/CMV] [other sequences ]			
<a href="#">Renilla luciferase reporter vector pGL4.75[hRluc/CMV], complete sequence</a>	228	5e-55	<a href="#">AY738231</a>
Renilla luciferase reporter vector pGL4.74[hRluc/TK] [other sequences ]			
<a href="#">Renilla luciferase reporter vector pGL4.74[hRluc/TK], complete sequence</a>	228	5e-55	<a href="#">AY738230</a>
Renilla luciferase reporter vector pGL4.73[hRluc/SV40] [other sequences ]			
<a href="#">Renilla luciferase reporter vector pGL4.73[hRluc/SV40], complete sequence</a>	228	5e-55	<a href="#">AY738229</a>
Renilla luciferase reporter vector pGL4.70[hRluc] [other sequences ]			
<a href="#">Renilla luciferase reporter vector pGL4.70[hRluc], complete sequence</a>	228	5e-55	<a href="#">AY738226</a>
Co-reporter vector phRG-TK [other sequences ]			
<a href="#">Co-reporter vector phRG-TK, complete sequence</a>	228	5e-55	<a href="#">AF362551</a>
Co-reporter vector phRG-B [other sequences ]			
<a href="#">Co-reporter vector phRG-B, complete sequence</a>	228	5e-55	<a href="#">AF362550</a>
Renilla luciferase reporter vector pGL4.82[hRluc/Puro] [other sequences ]			
<a href="#">Synthetic Renilla luciferase reporter vector pGL4.82[hRluc/Puro], complete sequence</a>	228	5e-55	<a href="#">DQ188846</a>
Renilla luciferase reporter vector pGL4.79[hRluc/Neo] [other sequences ]			
<a href="#">Renilla luciferase reporter vector pGL4.79[hRluc/Neo], complete sequence</a>	228	5e-55	<a href="#">DQ188843</a>
Luciferase reporter vector pGL4.76[hRluc/Hygro] [other sequences ]			
<a href="#">Luciferase reporter vector pGL4.76[hRluc/Hygro], complete sequence</a>	228	5e-55	<a href="#">AY864931</a>
Cloning vector pT7 RL2 [other sequences ]			
<a href="#">Cloning vector pT7 RL2, complete sequence</a>	217	1e-51	<a href="#">KM099240</a>
Cloning vector pT7_RL1 [other sequences ]			
<a href="#">Cloning vector pT7_RL1, complete sequence</a>	217	1e-51	<a href="#">KM099239</a>
Renilla luciferase reporter vector pGL4.72[hRlucCP] [other sequences ]			
<a href="#">Renilla luciferase reporter vector pGL4.72[hRlucCP], complete sequence</a>	217	1e-51	<a href="#">AY738228</a>
Renilla luciferase reporter vector pGL4.71[hRlucP] [other sequences ]			
<a href="#">Renilla luciferase reporter vector pGL4.71[hRlucP], complete sequence</a>	217	1e-51	<a href="#">AY738227</a>
Reporter vector phRG(R2.2) [other sequences ]			
<a href="#">Reporter vector phRG(R2.2), complete sequence</a>	217	1e-51	<a href="#">AY487824</a>
Reporter vector phRG(R2.1) [other sequences ]			
<a href="#">Reporter vector phRG(R2.1), complete sequence</a>	217	1e-51	<a href="#">AY487823</a>
Renilla luciferase reporter vector pGL4.84[hRlucCP/Puro] [other sequences ]			
<a href="#">Synthetic Renilla luciferase reporter vector pGL4.84[hRlucCP/Puro], complete sequence</a>	217	1e-51	<a href="#">DQ188848</a>
Renilla luciferase reporter vector pGL4.83[hRlucP/Puro] [other sequences ]			
<a href="#">Synthetic Renilla luciferase reporter vector pGL4.83[hRlucP/Puro], complete sequence</a>	217	1e-51	<a href="#">DQ188847</a>

Description	Score	E value	Accession
Renilla luciferase reporter vector pGL4.81[hRlucCP/Neo] [other sequences ]			
<a href="#">Synthetic Renilla luciferase reporter vector pGL4.81[hRlucCP/Neo], complete sequence</a>	217	1e-51	<a href="#">DQ188845</a>
Renilla luciferase reporter vector pGL4.80[hRlucP/Neo] [other sequences ]			
<a href="#">Synthetic Renilla luciferase reporter vector pGL4.80[hRlucP/Neo], complete sequence</a>	217	1e-51	<a href="#">DQ188844</a>
Luciferase reporter vector pGL4.78[hRlucCP/Hygro] [other sequences ]			
<a href="#">Luciferase reporter vector pGL4.78[hRlucCP/Hygro], complete sequence</a>	217	1e-51	<a href="#">AY864933</a>
Luciferase reporter vector pGL4.77[hRlucP/Hygro] [other sequences ]			
<a href="#">Luciferase reporter vector pGL4.77[hRlucP/Hygro], complete sequence</a>	217	1e-51	<a href="#">AY864932</a>
Plant expression vector pDuExB2 (pDuExD7) [other sequences ]			
<a href="#">Plant expression vector pDuExB2 (pDuExD7), complete sequence</a>	213	1e-50	<a href="#">EF565885</a>
Plant expression vector pDuExB (pDuExDc6) [other sequences ]			
<a href="#">Plant expression vector pDuExB (pDuExDc6), complete sequence</a>	213	1e-50	<a href="#">EF565884</a>
synthetic construct [other sequences ]			
<a href="#">Synthetic construct clone Den3-E24 Rluc-ubiquitin-neo fusion protein and polyprotein genes, complete cds</a>	211	5e-50	<a href="#">KM222446</a>
<a href="#">Synthetic construct clone Den3-E21 Rluc-ubiquitin-neo fusion protein and polyprotein genes, complete cds</a>	211	5e-50	<a href="#">KM222445</a>
<a href="#">Synthetic construct gene for mKusabiraOrangeKappa-RLuc8.6, complete cds</a>	206	2e-48	<a href="#">LC033422</a>
<a href="#">Synthetic construct gene for mKusabiraOrange1-RLuc8.6, complete cds</a>	206	2e-48	<a href="#">LC033416</a>
<a href="#">Synthetic construct gene for mCherry(delC13)-RLuc8.6(delN6), complete cds</a>	206	2e-48	<a href="#">LC033414</a>
<a href="#">Synthetic construct gene for mCherry(delC13)-RLuc8.6(delN5), complete cds</a>	206	2e-48	<a href="#">LC033413</a>
<a href="#">Synthetic construct gene for mCherry(delC13)-RLuc8.6(delN4), complete cds</a>	206	2e-48	<a href="#">LC033412</a>
<a href="#">Synthetic construct gene for mCherry(delC12)-RLuc8.6(delN6), complete cds</a>	206	2e-48	<a href="#">LC033411</a>
<a href="#">Synthetic construct gene for mCherry(delC12)-RLuc8.6(delN5), complete cds</a>	206	2e-48	<a href="#">LC033410</a>
<a href="#">Synthetic construct gene for mCherry(delC12)-RLuc8.6(delN4), complete cds</a>	206	2e-48	<a href="#">LC033409</a>
<a href="#">Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6(delN6), complete cds</a>	206	2e-48	<a href="#">LC033408</a>
<a href="#">Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6(delN5), complete cds</a>	206	2e-48	<a href="#">LC033407</a>
<a href="#">Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6(delN4), complete cds</a>	206	2e-48	<a href="#">LC033406</a>
<a href="#">Synthetic construct gene for mCherry(delC12)-delKpnI-RLuc8.6, complete cds</a>	206	2e-48	<a href="#">LC033405</a>
<a href="#">Synthetic construct gene for mCherry(delC10)-Orange-Nano-lantern, complete cds</a>	206	2e-48	<a href="#">LC033404</a>
<a href="#">Synthetic construct gene for Che(dC10-sC2)-RL8m1, complete cds</a>	206	2e-48	<a href="#">LC033401</a>
<a href="#">Synthetic construct gene for Che(dC10-sC1)-RL8m1, complete cds</a>	206	2e-48	<a href="#">LC033400</a>
<a href="#">Synthetic construct gene for Orange-Nano-lantern(Ca2+)-H2B, complete cds</a>	206	2e-48	<a href="#">AB983217</a>
<a href="#">Synthetic construct gene for Orange-Nano-lantern(Ca2+), complete cds</a>	206	2e-48	<a href="#">AB983216</a>
<a href="#">Synthetic construct gene for TurboFP650-RLuc8.6-545, complete cds</a>	206	2e-48	<a href="#">AB982104</a>
<a href="#">Synthetic construct gene for TurboFP635-RLuc8.6, complete cds</a>	206	2e-48	<a href="#">AB982103</a>
<a href="#">Synthetic construct gene for TurboFP635-RLuc8.6-545, complete cds</a>	206	2e-48	<a href="#">AB982102</a>
<a href="#">Synthetic construct gene for tdTomato-RLuc8.6, complete cds</a>	206	2e-48	<a href="#">AB982100</a>
<a href="#">Synthetic construct gene for TagRFP-RLuc8.6, complete cds</a>	206	2e-48	<a href="#">AB982098</a>
<a href="#">Synthetic construct gene for mRuby2-RLuc8.6, complete cds</a>	206	2e-48	<a href="#">AB982096</a>
<a href="#">Synthetic construct gene for mOrange2-RLuc8.6, complete cds</a>	206	2e-48	<a href="#">AB982095</a>
<a href="#">Synthetic construct gene for mKusabiraOrange2(delC5)-RLuc8.6, complete cds</a>	206	2e-48	<a href="#">AB982094</a>
<a href="#">Synthetic construct gene for mKusabiraOrange2(delC4)-RLuc8.6, complete cds</a>	206	2e-48	<a href="#">AB982093</a>



Description	Score	E value	Accession
Cloning vector pCRm-Rluc-PHLEO [other sequences ]			
<a href="#">Cloning vector pCRm-Rluc-PHLEO, complete sequence</a>	211	5e-50	<a href="#">KF035117</a>
Cloning vector pCRm-Rluc-PAC [other sequences ]			
<a href="#">Cloning vector pCRm-Rluc-PAC, complete sequence</a>	211	5e-50	<a href="#">KF035116</a>
Cloning vector pCRm-Rluc-NEO [other sequences ]			
<a href="#">Cloning vector pCRm-Rluc-NEO, complete sequence</a>	211	5e-50	<a href="#">KF035115</a>
Cloning vector pCRm-Rluc-HYG [other sequences ]			
<a href="#">Cloning vector pCRm-Rluc-HYG, complete sequence</a>	211	5e-50	<a href="#">KF035114</a>
Cloning vector pCRm-Rluc-BSD [other sequences ]			
<a href="#">Cloning vector pCRm-Rluc-BSD, complete sequence</a>	211	5e-50	<a href="#">KF035113</a>
Hepatitis C virus replicon 4a ED43-RlucNeo (R+I) [other sequences ]			
<a href="#">Hepatitis C virus replicon 4a ED43-RlucNeo (R+I), complete sequence</a>	211	5e-50	<a href="#">JX885981</a>
Biobrick cloning vector BBa_J96034 [other sequences ]			
<a href="#">Biobrick cloning vector BBa_J96034, complete sequence</a>	211	5e-50	<a href="#">JN204887</a>
Cloning vector pDuExDn6 [other sequences ]			
<a href="#">Cloning vector pDuExDn6, complete sequence</a>	211	5e-50	<a href="#">GU370779</a>
Cloning vector pBIND-GR [other sequences ]			
<a href="#">Cloning vector pBIND-GR, complete sequence</a>	211	5e-50	<a href="#">GQ229580</a>
Cloning vector pBIND-ER (alpha) [other sequences ]			
<a href="#">Cloning vector pBIND-ER (alpha), complete sequence</a>	211	5e-50	<a href="#">GQ229579</a>
Cloning vector pFN26A (BIND) hRluc-neo [other sequences ]			
<a href="#">Cloning vector pFN26A (BIND) hRluc-neo, complete sequence</a>	211	5e-50	<a href="#">GQ229578</a>
Cloning vector pmirGLO [other sequences ]			
<a href="#">Cloning vector pmirGLO, complete sequence</a>	211	5e-50	<a href="#">FJ376737</a>
CMV hRluc-neo Flexi Vector pF9A [other sequences ]			
<a href="#">CMV hRluc-neo Flexi Vector pF9A, complete sequence</a>	211	5e-50	<a href="#">DQ871024</a>

## ◦ Taxonomy

Taxonomy	Number of hits	Number of Organisms	Description
<a href="#">root</a>	<a href="#">101</a>	50	
. <a href="#">Muroidea</a>	<a href="#">30</a>	6	
.. <a href="#">Murinae</a>	<a href="#">25</a>	4	
... <a href="#">Mus</a>	<a href="#">21</a>	3	
.... <a href="#">Mus</a>	<a href="#">18</a>	2	
..... <a href="#">Mus musculus</a>	<a href="#">15</a>	1	<a href="#">Mus musculus hits</a>
..... <a href="#">Mus caroli</a>	<a href="#">3</a>	1	<a href="#">Mus caroli hits</a>
.... <a href="#">Mus pahari</a>	<a href="#">3</a>	1	<a href="#">Mus pahari hits</a>
... <a href="#">Rattus norvegicus</a>	<a href="#">4</a>	1	<a href="#">Rattus norvegicus hits</a>
.. <a href="#">Cricetinae</a>	<a href="#">5</a>	2	
... <a href="#">Mesocricetus auratus</a>	<a href="#">1</a>	1	<a href="#">Mesocricetus auratus hits</a>
... <a href="#">Cricetulus griseus</a>	<a href="#">4</a>	1	<a href="#">Cricetulus griseus hits</a>
. <a href="#">artificial sequences</a>	<a href="#">71</a>	44	

.. <a href="#">vectors</a>	<a href="#">43</a>	43	
... <a href="#">RNA interference vector psiCHECK(TM)-2</a>	<a href="#">1</a>	1	<a href="#">RNA interference vector psiCHECK(TM)-2 hits</a>
... <a href="#">RNA interference vector psiCHECK(TM)-1</a>	<a href="#">1</a>	1	<a href="#">RNA interference vector psiCHECK(TM)-1 hits</a>
... <a href="#">Co-reporter vector phRL-CMV</a>	<a href="#">1</a>	1	<a href="#">Co-reporter vector phRL-CMV hits</a>
... <a href="#">Co-reporter vector phRL-SV40</a>	<a href="#">1</a>	1	<a href="#">Co-reporter vector phRL-SV40 hits</a>
... <a href="#">Co-reporter vector phRL-TK(Int-)</a>	<a href="#">1</a>	1	<a href="#">Co-reporter vector phRL-TK(Int-) hits</a>
... <a href="#">Co-reporter vector phRL-null</a>	<a href="#">1</a>	1	<a href="#">Co-reporter vector phRL-null hits</a>
... <a href="#">Co-reporter vector pHRL-TK</a>	<a href="#">1</a>	1	<a href="#">Co-reporter vector pHRL-TK hits</a>
... <a href="#">Renilla luciferase reporter vector pGL4.75[hRluc/CMV]</a>	<a href="#">1</a>	1	<a href="#">Renilla luciferase reporter vector pGL4.75[hRluc/CMV] hits</a>
... <a href="#">Renilla luciferase reporter vector pGL4.74[hRluc/TK]</a>	<a href="#">1</a>	1	<a href="#">Renilla luciferase reporter vector pGL4.74[hRluc/TK] hits</a>
... <a href="#">Renilla luciferase reporter vector pGL4.73[hRluc/SV40]</a>	<a href="#">1</a>	1	<a href="#">Renilla luciferase reporter vector pGL4.73[hRluc/SV40] hits</a>
... <a href="#">Renilla luciferase reporter vector pGL4.70[hRluc]</a>	<a href="#">1</a>	1	<a href="#">Renilla luciferase reporter vector pGL4.70[hRluc] hits</a>
... <a href="#">Co-reporter vector phRG-TK</a>	<a href="#">1</a>	1	<a href="#">Co-reporter vector phRG-TK hits</a>
... <a href="#">Co-reporter vector phRG-B</a>	<a href="#">1</a>	1	<a href="#">Co-reporter vector phRG-B hits</a>
... <a href="#">eukaryotic vectors</a>	<a href="#">6</a>	6	
.... <a href="#">Renilla luciferase reporter vector pGL4.82[hRluc/Puro]</a>	<a href="#">1</a>	1	<a href="#">Renilla luciferase reporter vector pGL4.82[hRluc/Puro] hits</a>
.... <a href="#">Renilla luciferase reporter vector pGL4.79[hRluc/Neo]</a>	<a href="#">1</a>	1	<a href="#">Renilla luciferase reporter vector pGL4.79[hRluc/Neo] hits</a>
.... <a href="#">Renilla luciferase reporter vector pGL4.84[hRlucCP/Puro]</a>	<a href="#">1</a>	1	<a href="#">Renilla luciferase reporter vector pGL4.84[hRlucCP/Puro] hits</a>
.... <a href="#">Renilla luciferase reporter vector pGL4.83[hRlucP/Puro]</a>	<a href="#">1</a>	1	<a href="#">Renilla luciferase reporter vector pGL4.83[hRlucP/Puro] hits</a>
.... <a href="#">Renilla luciferase reporter vector pGL4.81[hRlucCP/Neo]</a>	<a href="#">1</a>	1	<a href="#">Renilla luciferase reporter vector pGL4.81[hRlucCP/Neo] hits</a>
.... <a href="#">Renilla luciferase reporter vector pGL4.80[hRlucP/Neo]</a>	<a href="#">1</a>	1	<a href="#">Renilla luciferase reporter vector pGL4.80[hRlucP/Neo] hits</a>
... <a href="#">Luciferase reporter vector pGL4.76[hRluc/Hygro]</a>	<a href="#">1</a>	1	<a href="#">Luciferase reporter vector pGL4.76[hRluc/Hygro] hits</a>
... <a href="#">Cloning vector pT7 RL2</a>	<a href="#">1</a>	1	<a href="#">Cloning vector pT7 RL2 hits</a>
... <a href="#">Cloning vector pT7 RL1</a>	<a href="#">1</a>	1	<a href="#">Cloning vector pT7 RL1 hits</a>
... <a href="#">Renilla luciferase reporter vector pGL4.72[hRlucCP]</a>	<a href="#">1</a>	1	<a href="#">Renilla luciferase reporter vector pGL4.72[hRlucCP] hits</a>
... <a href="#">Renilla luciferase reporter vector pGL4.71[hRlucP]</a>	<a href="#">1</a>	1	<a href="#">Renilla luciferase reporter vector pGL4.71[hRlucP] hits</a>
... <a href="#">Reporter vector phRG(R2.2)</a>	<a href="#">1</a>	1	<a href="#">Reporter vector phRG(R2.2) hits</a>
... <a href="#">Reporter vector phRG(R2.1)</a>	<a href="#">1</a>	1	<a href="#">Reporter vector phRG(R2.1) hits</a>
... <a href="#">Luciferase reporter vector pGL4.78[hRlucCP/Hygro]</a>	<a href="#">1</a>	1	<a href="#">Luciferase reporter vector pGL4.78[hRlucCP/Hygro] hits</a>
... <a href="#">Luciferase reporter vector pGL4.77[hRlucP/Hygro]</a>	<a href="#">1</a>	1	<a href="#">Luciferase reporter vector pGL4.77[hRlucP/Hygro] hits</a>
... <a href="#">Plant expression vector pDuExB2 (pDuExD7)</a>	<a href="#">1</a>	1	<a href="#">Plant expression vector pDuExB2 (pDuExD7) hits</a>
... <a href="#">Plant expression vector pDuExB (pDuExDc6)</a>	<a href="#">1</a>	1	<a href="#">Plant expression vector pDuExB (pDuExDc6) hits</a>
... <a href="#">Cloning vector pCRm-Rluc-PHLEO</a>	<a href="#">1</a>	1	<a href="#">Cloning vector pCRm-Rluc-PHLEO hits</a>
... <a href="#">Cloning vector pCRm-Rluc-PAC</a>	<a href="#">1</a>	1	<a href="#">Cloning vector pCRm-Rluc-PAC hits</a>
... <a href="#">Cloning vector pCRm-Rluc-NEO</a>	<a href="#">1</a>	1	<a href="#">Cloning vector pCRm-Rluc-NEO hits</a>
... <a href="#">Cloning vector pCRm-Rluc-HYG</a>	<a href="#">1</a>	1	<a href="#">Cloning vector pCRm-Rluc-HYG hits</a>

... <a href="#">Cloning_vector pCRm-Rluc-BSD</a>	<a href="#">1</a>	1	<a href="#">Cloning_vector pCRm-Rluc-BSD hits</a>
... <a href="#">Hepatitis C virus replicon 4a ED43-RlucNeo (R+I)</a>	<a href="#">1</a>	1	<a href="#">Hepatitis C virus replicon 4a ED43-RlucNeo (R+I) hits</a>
... <a href="#">Biobrick cloning vector BBa_J96034</a>	<a href="#">1</a>	1	<a href="#">Biobrick cloning vector BBa_J96034 hits</a>
... <a href="#">Cloning_vector pDuExDn6</a>	<a href="#">1</a>	1	<a href="#">Cloning_vector pDuExDn6 hits</a>
... <a href="#">Cloning_vector pBIND-GR</a>	<a href="#">1</a>	1	<a href="#">Cloning_vector pBIND-GR hits</a>
... <a href="#">Cloning_vector pBIND-ER (alpha)</a>	<a href="#">1</a>	1	<a href="#">Cloning_vector pBIND-ER (alpha) hits</a>
... <a href="#">Cloning_vector pFN26A (BIND) hRluc-neo</a>	<a href="#">1</a>	1	<a href="#">Cloning_vector pFN26A (BIND) hRluc-neo hits</a>
... <a href="#">Cloning_vector pmirGLO</a>	<a href="#">1</a>	1	<a href="#">Cloning_vector pmirGLO hits</a>
... <a href="#">CMV hRluc-neo Flexi Vector pF9A</a>	<a href="#">1</a>	1	<a href="#">CMV hRluc-neo Flexi Vector pF9A hits</a>
.. <a href="#">synthetic construct</a>	<a href="#">28</a>	1	<a href="#">synthetic construct hits</a>

Top